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GenCore version 5.1.3
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	DNA sequence encod DNA encoding human Codon-optimised RA Human alpha-1-tryb
SUMMARIES	ABK88025 ABK88027 ABK88026 ABK8022 ABK88023 ABK88024 ABK88015 AAV41730 AAV41730
DB	2222222 222222222222222222222222222222
Query Guery e Match Length DB	1525 1582 1756 1756 1756 1182 1182 1312
% Query Match	100.00 78.55 78.17 78.17 77.88 77.58 41.22
Score	1525 1197.4 1191.6 1191.6 1188.8 1187 1182 628.4
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01111111111111111111111111111111111111	0 T T T T T T T T T T T T T T T T T T T

## ALIGNMENTS

rSLAP1; gene; ds; Alzheimer's disease; tumour anglogenesis; malaria; emphysems; asthma; chronic obstructive pulmonary disease; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; muscular dystrophy; tumour metastasis; osteoporosis; paget's disease; scleroderma; glomerulonephritis; hypertension. /\*tag= a /standard\_name= "Ribosome binding site" /product= "rSLAP1 fusion protein" DNA sequence encoding rSLAP1 fusion protein. /\*tag= c /note= "AAT coding region" 1194..1196 Location/Qualifiers ABK88025 standard; DNA; 1525 (first entry) \*tag= b 12..1193 ..1520 /\*tag= Homo sapiens. Synthetic. misc\_feature misc\_feature 07-OCT-2002 ABK88025; RESULT 1 ABK8802 

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This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor of its functionally active portion and relation proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention of the invention as an enhibitor of protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, such as emphysema, asthma, chronic obstructive pulmonary disease, such as emphysema, outlis media ottis external or HIV infection, or for treating an individual suffering from or at risk for a disease or for treating dermatological diseases such as atopic dermatitis, eccemna of proteins are useful sead proteins are useful in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic treating herpes infection, corneal or epidermal ulceration, chronic treating herpes are activity; periodontal disease, the management of the proteins of the proteins are useful and proteins are such as a protein and for the proteins are useful and proteins are are also and proteins are are activity, and proteins are are activity and proteins are are activity and and proteins are are activity and proteins are are activity and proteins are activity and proteins are activity and proteins are activity and activity are activity and activity and activity and activity and activity a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
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241 TAGAAGGTTTAAACTTTAATTTGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTC 300
                         AAGAGTICITGAGAACTITGAATCAACCTGAITCTCAAITGCAAITAACTACTGGIAACG 360
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malaria; emphysema; asthma; chronic obstructive purposations; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; osteoporosis; Paget's disease; scleroderma; glomerulonephritis; hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor.
GTAAGTGTCCAGTTACTTACGTCAATGTTTGATGTTGAACCCACCAAACTTCTGTGAAA 1440
             1381 GTAAGTGTCCAGTTACTTACGGTCAATGTTTGATGTTGAACCCACCAACTTCTGTGAAA 1440
                                                TGGACGGTCAATGTAAGAGACTTGAAGTGTTGTATGGGTATGTGTGGTAAGTCCTGTG 1500
                                                                        rN-TAP1; gene; ds; Alzheimer's disease; tumour angiogenesis; malaria; emphysema; asthma; chronic obstructive pulmonary di
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/standard_name= "Ribosome binding site"
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                                                                                                                                                                                                                                                             DNA sequence encoding rN-TAP1 fusion protein.
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/note= "AAT coding region"
1194..1196
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procease inhibitor comprising an alphal-antitypsin or its functionally active portion and a second procease inhibitor or its functionally active portion and a second procease inhibitor or its functionally active portion and a second procease inhibitor or its functionally active protein. The fusion process of the invention may act as an inhibitor of procease activity associated with a disorder is useful for inhibiting procease activity associated with a disorder cystic fibrosis, ottis media, othis external or HY infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted procease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema sor inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepais, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, chronic conhealing wounds, sepais, rheumatoid arthritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular reverse in the present sequence represents the DNA encoding the
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1582 BP; 464 A; 334 C; 329 G; 455 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1197.4; DB 20
Pred. No. 5.5e-291;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                 rN-TAP1 fusion protein of the invention.
Example 3; Page 95-96; 134pp; English.
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99.9%;
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malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; osteoporosis; Paget's disease; scleroderma; glomerulonephritis; hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTTAACTATTGATGAAAAGGGTACCGAGGCCGCGGCGCCTATGTTCTGGAAGCTATTC 1080
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                                                                                  rTAP1; gene; ds; Alzheimer's disease; tumour angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name= "Ribosome binding site"
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/note= "TIMP-1 coding region"
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'note= "AAT coding region"
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'note= "linking codon"
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and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rhewmatoid arthritis, periodontal disease, tumnour metastasis and tumnour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                              protease inhibitor comprising an alphal-antitypsin or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema
                                                                                                                                                                                                                                                                                                     Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
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Best Local Similarity 99.9%;
Matches 1198; Conservative
                                                                                   18-DEC-2001; 2001WO-US49256
                                                                                                                                           20-NOV-2001; 2001US-331966P
                                                                                                                        18-DEC-2000; 2000US-256699P
                                                                                                                                                                             (ARRI-) ARRIVA PHARM INC.
                                                                                                                                                                                                                 Barr PJ, Gibson HL,
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                                                                                                                                                                                                                                                                        P-PSDB; AAU99889
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Yeast; alpha factor; gene; ds; Alzheimer's disease; SLAPI; malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
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                                                    TTAATGATTATGTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAG 540
                                                                                                                                      CTTTCGAGGTTAAAGATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCA 660
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GTTTATTTTTGTCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAAC
                                                                                             CTTTCGAGGTTAAAGATACTGAAGAGGAAGTTTTCATGTTGATCAAGTTACTACTGTGA
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                                                                                                                                                                                                             AAGTTCCAATGATGAAAAGACTGGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTT
                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence encoding SLAP1 fusion protein.
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This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portion and a second protease activity and a second protease activity is a social for inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, costic fibrosis, otitis media otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic transming wounds, sepsis, rheumatoid arthritis, periodontal disease, tuniour metastasis and tumour angiogenesis, gastric ulceration, maineds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, sclaroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the
tumour metastasis; tumour anglogenesis; osteoporosis; Paget's disease;
glomerulonephritis; scleroderma; hypertension.
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/standard_name= "Ribosome binding site"
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Best Local Similarity 99.7%; Pred. No. 1.6e-289;
Matches 1194; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                 "SLAP1 fusion protein"
                                                                                                                                                                                                                                                       SLPI coding region
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/note= "linking codon"
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                                                                                                        Cocation/Qualifiers
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1405 CAATGAGCATTCCACCAGAAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATCGAGC 1464

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CAATGAGCATTCCACCAGAAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATCGAGC 1140
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                                         ACCAAGACCATCCGACTTTTAATAAAATTACTCCAAATTTAGCCGAATTTGCTTTTTCTT
                                                                                                               TIGCCACTGCTTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTT
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This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention
                                                                                                                                                                                        TAP1; gene; ds; Alzheimer's disease; tumour angiogenesis; malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes, ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; osteoporosis; Paget's disease; scleroderma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
/*tag= a
/standard_name= "Ribosome binding site"
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"TIMP-1 coding region"
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                                                                                                                                                                  DNA sequence encoding TAP1 fusion protein.
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/note= "linking codon"
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                                                                                                                                                                                                                                                                    glomerulonephritis; hypertension.
                                                                                      BP.
                                                                                      DNA; 1756
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2001US-331966P.
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                                                                                                                                         (first entry)
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                                                                                      ABK88023 standard;
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20-NOV-2001;
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                                                                                                                                                                                                                                                                                                         Synthetic.
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such as emphysema, asthma, forcolc obstructive pulmonary disease, cystic fibrosis, otitis media, otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, obsteoporosis, paget's disease, glomerulonephitiis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular TAPI fusion protein of the invention.
useful for inhibiting protease activity associated with a disorder
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Sequence 1756 BP; 493 A; 395 C; 373 G; 495 T; 0 other;

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                                        7 CCATGGAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACACCAGTCATCACGACCAAG
                                                                                                                                                                     CTGCTTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAG
                                                                                                                                                                                TGTTGAGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTAT
                                                                                                                                                                                                                                                                1222 CAATGATGAAAAGACTGGGTATGATTCAATATTCAACATTGCAAAAATTAAGTTCTTGGG
                                                                                                                                                                                                             GTTTAAACTTTAATTTGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTCAAGAGT
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   24; Length 1756;
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                      Indels
 Score 1188.8; DB 24
Pred. No. 8.3e-289;
                    0; Mismatches
Ouery Match
Best Local Similarity 99.8%;
Matches 1190; Conservative
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18-DEC-2001; 2001WO-US49256

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NTAP1; gene; ds; Alzheimer's disease; tumour angiogenesis; malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; osteoporosis; Paget's disease; scleroderma;
                                                                                           1642 GCATTCCACCAGAAGTTAAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACA 1701
             GIGGIGITACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAA 1026
                                                                                                                                                                                        CTATTGATGAAAAGGGTACCGAGGCCGCCGCGCCTATGTTCCTGGAAGCTATTCCAATGA 1086
                                                                                                                                                                                                                                      GCATTCCACCAGAAGTTAAATTTAATAAACCATTCGTTTTTTCTGATGATGAGCAGAACA 1146
                                               AGGATCGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACGGTACTTACGACT 906
  AGCTTCAACATTTAGAGAATGAGTTGACTCATGACATTATTACTAAATTTTTAGAGAACG
                                                          1147 CTAAAAGCCCATTGTTATGGGTAAGGTTGTCAACCCAACTCAGAAGATGTC 1198
                                                                                                                                                                                                                                                                                               1702 CTAAAAGCCCATTGTTTATGGGTAAGGTTGTCAACCCAACTCAGAAGTAGTC 1753
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/standard_name- "Ribosome binding site"
}..1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "NTAP1 fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= c
/note= "TIMP-1 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence encoding N-TAP1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "AAT coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glomerulonephritis; hypertension.
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/note= "linking
                                                                                                                                                                                                                                                                                                                                                                     ABK88024 standard; DNA; 1582
                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag- b
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This invention relates to a novel fusion protein comprising a first

protease inhibitor comprising an alphal-antitrypsin or its functionally

cative portion and a second protease inhibitor or its functionally

active protein. The fusion proteins of the invention may act as an

cative protein. The fusion protein of the invention

is useful for inhibiting protease activity associated with a disorder

cation as emphysema, asthma, chronic obstructive pulmonary disease,

cystic fibrosis, oftits media, oftits external or HIV infection, or

cystic fibrosis, oftits media, oftits external or HIV infection, or

cystic fibrosis, oftits media, oftits external or HIV infection, or

consider involving unwanted protease activity. The proteins are useful

consider involving unmanted proteases such as actopic dermatitis, eczema

con psortasis, in inflammatory responses to viral infection, and for

treating herpes infection, corneal or epidermal ulceration,

creating herpes and tumour angiogenesis, agastric ulceration,

con non-healing wounds, sepsis, rhematoid arthritis, periodontal disease,

connection, paget's disease, glomerulonephritis, scleroderma, malaria,

conservation infection, Alzheimer's disease, hypertension and muscular

conservation in the present sequence represents the DNA encoding the
                                                                                                                                                                                              Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCATAGTGAGGCTTTTACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 AGGAAATGGAAGACCCTCAAGGCGACGCCGCTCAAAAACCGACACCAGTCATCACGACC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGACCAICCGACIITIAAIAAAAITACICCAAAIITAGCCGAAITIGCIITITCIIIGI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AIAGACAATIAGCICAICAAAGIAAIICIACIAACAITITITITAGICCIGIIICIAIIG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACTGCTTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 AAGGITITAAACTITAAATITGACCGAAAICCCAGAAGCCCAAATICACGAGGGITITCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          685 AGTIGITGAGAACTITGAATCAACCIGAITCTCAATIGCAATTAACTACTGGTAACGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 IAITITIGICIGAAGGITIAAAATIGGITGACAAATICCIAGAAGACGICAAGAAACIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 AGTIGITGAGAACTITGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1582 BP; 464 A; 333 C; 329 G; 456 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.8%; Score 1187; DB 24;
99.6%; Pred. No. 2.3e-288;
tive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTAP1 fusion protein of the invention.
                                                                                                                                                                                                                                                                                                      Example 2; Page 85-86; 134pp; English.
                                                                                                 Pemberton P;
18-DEC-2000; 2000US-256699P.
20-NOV-2001; 2001US-331966P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.6
Matches 1190; Conservative
                                                           (ARRI-) ARRIVA PHARM INC
                                                                                                   Gibson HL,
                                                                                                                                            2002-500631/53
                                                                                                                                                               P-PSDB; AAU99883
                                                                                                                                                                                                                                                                    inhibitor
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                                                                                                   Barr PJ,
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Alpha-1-antitrypsin; AAT; human; gene; ds; protease inhibitor; malaria;
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805 ATCATAGTGAGGCTTTTACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTA 864
                                                                                                                                                                                                                                                                                                                                    964 IGAGIGGIGITACIGAAGAAGCICCATIAAAAITGAGIAAAGCIGIICACAAAGCCGICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1024 TAACTATIGATGAAAAGGGTACCGAGGCCGCCGCGCGTATGTTCCTGGAAGCTATTCCAA
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                                                                                                                                                                                                                                  ATGATTATGTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATC
                                    GIGATACCGTCTTCGCACTAGTTAACTATTTTTTTCAAGGGTAAGTGGGAACGTCCTT
                                                                                                    925 GIGATACCGICITCGCACIAGITAACIAITITITITTAGGGGTAAGIGGGAACGICCII
                                                                                                                              TCGAGGTTAAAGATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAG
                                                                                                                                                                              664 IICCAAIGAAAAGACIGGGIAIGIICAAIAITCAACAIIGCAAAAAIIAAGIICII
                                                                                           DNA encoding human alpha-1-antitrypsin (AAT) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 GAAGACCCTCAAGGCGACGCCGCTCAAAAACCGACACCAGTCATCACGACCAAGACCAT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 77.5%; Score 1182; DB 24; Length 1182; Local Similarity 100.0%; Pred. No. 3.7e-287; nes 1182; Conservative 0; Mismatches 0; Indels 0;
/*tag= a
/product= "Alpha-1-antitrypsin"
/partial
/note= "No start or stop codon shown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1182 BP; 369 A; 214 C; 229 G; 370 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 24-25; 134pp; English.
                                                                                                                                                                                                                                                               Pemberton P;
                                                                                                                                             18-DEC-2001; 2001WO-US49256.
                                                                                                                                                                             18-DEC-2000; 2000US-256699P. 20-NOV-2001; 2001US-331966P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 1182; Conservative
                                                                                                                                                                                                                            (ARRI-) ARRIVA PHARM INC
                                                                                                                                                                                                                                                          Barr PJ, Gibson HL,
                                                                                                                                                                                                                                                                                           2002-500631/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention
                                                                              WO200250287-A2
                                                                                                             27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                         inhibitor
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241 AACTTTAATTTGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTTG 300
                                                                                                                                                                                                                                                                                                                                   661 ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA 720
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                                                                    372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT
                                                                                                                  432 GAGGCTTTTACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT
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                                                                                                                                                                 492 GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAAGAATTAGATCGTGATACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Codon-optimised RAmy3D signal fused to DNA encoding mature AAT.
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          glycosylated alpha 1-antitrypsin; AAT; glycosylated antithrombin III; ATIII; human serum albumin; HSA; subtilisin BPN'; treatment; emphysema; antithrombotic; blood replacement; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 CCGACTTTTAATAAATTACTCCAAATTTAGCCGAATTTGCTTTTTCTTTGTATAGACAA 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressing mature, glycosylated proteins in monocotyledonous plant cells - from chimeric gene including signal peptide sequence, specifically therapeutic agents and industrial enzymes
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"codon-optimised RAmy3D signal sequence"
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Protein expression; monocotyledon plant cell;
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                                                                                                           Location/Qualifiers
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                                                                    TICGCCATGITGAGITITAGGIACIAAAGCCGATACCCAIGACGAGAITITAGAAGGITIA
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1000 AGCGTCCTAGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGG 1059
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                    400 CGTACCCTCAACCAGCCAGACAGCTCCAGCTGACCACCGGCAATGGCCTGTTCCTC 459
                                                                                                                                       312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTG 371
                                                                                                                       372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 28.3%; Score 432.2; DB 16; Length 1312; Best Local Similarity 60.4%; Pred. No. 1.1e-98; Matches 713; Conservative 0; Mismatches 468; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTTTAGTCCTGTTTCTATTGCCACTGCT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACACCAGTCATCACGACCAAGACCAT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of a human alpha-1-antitrypsin cDNA clone is given iAA089254. Expression of the cDNA in host cell transformants has allowed production of recombinant alpha-1-antitrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human alphal-antitrypsin (al-AT) cDNA sequence - can be used for the expression of al-AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1312 BP; 339 A; 368 C; 324 G; 281 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WOO SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davie EW, Kurachi K, Thirumalachary C,
                                                                                                   Alpha-1-trypsin; protease-inhibitor; ss
                                                                                                                                                     Location/Qualifiers
28..1258
  AAQ89254 standard; cDNA; 1312 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig.1; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                      87US-0131190.
88US-0246912.
89US-0398288.
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84US-0638980.
87US-0022543.
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92US-0979556
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                                                  (first entry)
                                                                            Human alpha-1-trypsin cDNA
                                                                                                                                                                            /*tag a 28..99 /*tag b 100..1255 /*tag c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-130740/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR71969
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18-NOV-1992;
02-JUL-1993;
                                                                                                                            Homo saptens
                                                    18-OCT-1995
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312 AGAACTTTGAATCAACTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTG 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 ccaaccricaacaagarcaccccaacriggcrgagricgccricagccraraccgccag 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 ITAGCTCATCAAAGTAATTCTACTAACATTTTTTTTAGTCCTGTTTCTATTGCCACTGCT 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 ITCGCCATGTTGAGTTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTA
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                                                          Human alpha-1-antitrypsin; ATR-1; antibody; ATR-1 deficiency; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding alpha-1 anti-trypsin - useful for, e.g. producing recombinant alpha-1 anti-trypsin
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0; Mismatches 468; Indels
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                                                                                                                                                               /*tag= a
/product= "alpha-1-antitrypsin"
                             Nucleotide sequence of the alpha-1-antitrypsin
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                                                                                                                        Location/Qualifiers
28..1257
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87US-0133190.
88US-0246912.
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92US-0979556.
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18-NOV-1992;
02-JUL-1993;
                                                                                                     Homo sapiens
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16-SEP-1988;
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972 GITACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATT 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1180 CGCCCCGAGGTCAAGTTCAACAAACCCTTTGTCTTTAATGATTGAAGAAATACCAAG 1239
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                                                                                                                                                                                                                                                                                                                       672 ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA 731
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                                                                 580 GIGGAGAAGGGIACTCAAGGAAAAITGTGGATTIGGTCAAGGAGCTTGACAGAGACAA 639
                                                                                                                                                                                                                                                                                                                                                                                     671
400 ceraccercaaccagacagacagceagcecagergacacaggaarggcergreere 459
                                                                                                                             GAGGCTTTTACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT 491
                                                                                                                                                                                                              GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC 551
                                         372 ICIGAAGGITIAAAAITGGITGACAAAITCCIAGAAGACGICAAGAAACIAIAATCAIAGI 431
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sequence. Alphal-antitrypsin is an important protease inhibitor, the major function of which is to inhibit neutrophil elastase. Low levels of alphal-antitrypsin in the blood are associated with chronic obstructive pulmonary emphysema and infantile liver cirrhosis. A vector comprising a mammalian alphal-antitrypsin DNA sequence that hybridises to human alphal-antitrypsin cDNA can be introduced into a host cell in a method for the production of alphal-antitrypsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the human alphal-antitrypsin nucleotide
                                                                                                                                                                                                                                                                                                                                                                                        Preparing alphal-antitrypsin for inhibiting neutrophil elastase involves transfecting host cell with vector comprising alphal-antitrypsin DNA sequence that hybridizes to human alphal-antitrypsin cDNA, or its complement -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1312 BP; 339 A; 368 C; 324 G; 281 T; 0 other;
                                                                                                                                                                                                                                                                                                                        Davie EW;
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92US-0979556.
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84US-0638980
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87US-0133190
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89US-0398288
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                Homo saptens
                                         US6025161-A.
                                                                                                  20-JAN-1998;
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1060 GTCACAGAGGAGGCACCCCTGAAGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCATC 1119
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                        492 GITGAGAAAGGCACCCAGGGTAAGAICGTIGACCTAGTIAAAGAATTAGAICGTGAIACC 551
                                                                                                                                                                                                              GTGGAGAAGGCTACTCAAGGGAAAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACA 639
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372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT 431
                                                                                                                                                                                                                                                                                                                                                                                                                          672 ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection;
                                                                                                              GAGGCTTTTACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT
                                                                                                                                                                                                                                                      GTCTTCGCACTAGTTAACTATTTTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTT
                                                                                                                                                                                                                                                                                                                                       612 AAAGATACTGAAGAAGAATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG
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Mon Dec

The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating the invention relates to novel isolated human secreted polypeptides (II). (I) and modilators of ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopolesis, stem cell survival, bone growth and remodeling. (II) and modilators of (II) are useful for and remodeling. (II) and modilators of (II) are useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modilators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and and brain tissue and is useful for the treatment of central and and brain tissue and is useful for the treatment of central and and brain tissue and is useful for the treatment of central and activity, regulation of haematopolesis and is useful for treating myeloid cell disorders, platelet disorders such as thrombocytopenia or lympholi cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incissue content and or regeneration and treatment of lung or liver fibrosis, cuperfusion injury in various tissues, various immune deficiencies and conditions, such manned discaes. Purthermore, (I) is also useful for for regeneration and treatment of lung or liver fibrosis. Fibrumatoid arthritis, diabetes mellitus, mysathenia gravis, allergic reperfusion injury in various tissues, various immune deficiencies and conditions, such as asthma or other respiratory problems. Creations and conditions, such as asthma or other respiratory problems. Creations and conditions, such as asthma or other respiratory manned and an act as an antigen or circade proposition, carbohlydrate, vitamins, immune respiration or ther invention and expense. Assidion o Zhou P; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J; fertility; analgesic; pain; antigen; ss. Claim 1; SEQ ID No 133; 107pp; English. coding sequences of the invention. 19-MAY-2000; 2000US-0574454. 17-JUN-2000; 2000US-0596193. 14-JUL-2000; 2000US-0616847. 19-SEP-2000; 2000US-0665363. 20-OCT-2000; 2000US-0693267. Liu C, Asundi V, Yang Y, Drmanac R 05-MAR-2001; 2001WO-US04942 07-MAR-2000; 2000US-0519705 WPI; 2001-589934/66. (HYSE-) HYSEQ INC. P-PSDB; AAU28152 WO200166689-A2 Homo sapiens. 13-SEP-2001, Zhao QA, rang YT,

Gaps DB 22; Length 1367; 1; 28.1%; Score 429.2; DB 22; Length 60.7%; Pred. No. 6.6e-98; Live 0; Mismatches 463; Indels Sequence 1367 BP; 357 A; 392 C; 323 G; 295 T; 0 other; Best Local Similarity 60.7 Matches 718; Conservative Query Match

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971 IGTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTAT 1030 TGATGAAAAGGGTACCGAGGCCGCCGCGCTATGTTCCTGGAAGCTATTCCAATGAGCAT 1090 1091 TCCACCAGAAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAA 1150 1065 GGTCACAGAGGAGGCACCCTGAAGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCAT 1124 945 CAGAAGGICIGCCAGCITACATITACCCAAACIGICCATIACIGGAACCIAIGAICIGAA 1004 1005 GAGCGICCIGGGICAACIGGGCAICACIAAGGICIICAGCAAIGGGGCIGACCICICCGG 1064 910 730 790 610 764 884 252 AACTITAATITIGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTTG 311 432 GAGGCTTTTACCGTTAATTTTGGTGAT-ACTGAGGAAGCTAAAAAGCAAATTAATGATTA 490 IGTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATAC 550 704 285 TITICCAATGCTCCCCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTG 344 312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTG 371 372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT 431 165 CCAACCTICAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAG 224 225 CIGGCACACCAGICCAACAGCACCAATAICTICTICTCCCCAGIGAGCAICGCIACAGCC 284 12 GAAGACCCTCAAGGCGACGCCGCTCAAAAACCGACACCAGTCATCACGACCAAGACCAT 71 525 GAAGCCTTCACTGTCAACTTCGGGGATCACCGAAGAGGCCCAAGAACAGATCAACGATTA 551 CGTCTTCGCACTAGTTAACTATTTTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGT 671 GATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAAATTAAGTTCTTGGGTCTT 611 TAAAGATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAAT 791 TCAACATTTAGAGAATGAGTTGACTCATGACATTATTACTAAATTTTTAGAGAACGAGGA 851 TCGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAA 132 ITAGCTCATCAAAGTAATTCTACTAACATTTTTTTTAGTCCTGTTTCTATTGCCACTGCT 345 AATITCAACCICACGGAGAIICCGGAGGCICAGAICCAIGAAGGCIICCAGGAACICCIC 192 TICGCCATGITGAGITTAGGIACIAAAGCCGAIACCCAIGACGAGAITITAGAAGGIITA 491 П q δò g ŏ В òγ g qq g ò g ğ ŏ g g δ ద ò ð g δ ò g δ ŏ ö δ g

1245 GTCTCCCTCTTCATGGGAAAGTGGTGAATCCCACCAAAA 1286 1151 AAGCCCATTGTTATGGGTAAGGTTGTCAACCCCAACTCAGAA 1192 ð

## RESULT 13 AAV41726

AAV41726 standard; DNA; 1185 BP

AAV41726;

(first entry) 20-NOV-1998

Native coding sequence of mature alphal-antitrypsin (AAT).

Protein expression; monocotyledon plant cell; glycosylated antithrombin III; glycosylated abpa i-antitrypsin; AAT; glycosylated antithrombin III; ATIII; human serum albumin; HSA; subtilisin BPN'; treatment; emphysema; antithrombotic; blood replacement; ss.

Homo sapiens

20-AUG-1998

98WO-US03068 13-FEB-1998;

97US-0038170. 97US-0037991. 97US-0038168. 97US-0038169. 3-FEB-1997; 13-FEB-1997;

13-FEB-1997; 3-FEB-1997;

PHYT-) APPLIED PHYTOLOGICS INC.

Sutliff TD; Rodriguez RL,

WPI; 1998-467179/40. P-PSDB; AAW59839. Expressing mature, glycosylated proteins in monocotyledonous plant cells - from chimeric gene including signal peptide sequence, specifically therapeutic agents and industrial enzymes

Disclosure; Page 29; 53pp; English.

The present sequence represents the native coding sequence of mature alphai-antitrypsin (AAT). The protein is used to exemplify the alphai-antitrypsin (AAT). The protein is used to exemplify the network of the specification describes method for producing mature beterologous protein in monocotyledonous plant cells. The method comprises transforming the cells with a chimeric gene comprising a monocotyledon transcription regulator, inducible either during seed maturation or by adding/removing a small molecule, DNA encoding the the signal peptide causing secretion of the protein from the cell. Proteins expressed in this manner include mature glycosylated alpha increases its serum half-life, mature glycosylated antithrombin in cases its serum half-life, mature glycosylated antithrombin in (ATII), mature human serum albuing characteristics, or mature active subtilisin BPN'. These protein from the respective subtilisin BPN'. These proteins are useful therapeutically (e.g. AAT for treating emphysema, ATIII as antithrombotic and HSA as blood replacement) or as industrial enzymes (BPN' is used in detergents). 

Sequence 1185 BP; 328 A; 324 C; 283 G; 250 T; 0 other;

ö Gaps ö Query Match 28.1%; Score 429; DB 19; Length 1185; Best Local Similarity 60.2%; Pred. No. 7.1e-98; Matches 711; Conservative 0; Mismatches 470; Indels 0

972 GTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTAT 1031 1092 CCACCAGAAGTTAAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAA 1151 131 251 311 300 371 540 301 CGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCTGACCACCGGCAATGGCCTGTTCCTC 360 491 551 611 9 671 999 372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT 431 GAAGCCTTCACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACGATTAC 480 731 791 851 911 900 971 CCGACTTTTAATAAAATTACTCCAAATTTAGCCGAATTTGCTTTTTCTTTGTATAGACAA 121 CTGGCACACCAATCACCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGC TTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTA **AACTITAATITIGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTTG** 312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTG GTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTTGGTCAAGGAGCTTGACAGAGACACA TTAGCTCATCAAAGTAATTCTACTAACATTTTTTTTAGTCCTGTTTCTATTGCCACTGCT GAAGACCCTCAAGGCGACGCCGCTCAAAAACCGACACCAGTCATCACGACCAAGACCAT GTCTTCGCACTAGTTAACTATTTTTTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTT AAAGATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA 841 AGAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAG GAGGCTTTTACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC 792 CAACATTTAGAGAATGAGTTGACTCATGACATTATTACTAAATTTTTAGAGAACGAGGAT 852 CGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAA 912 TCTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTTTTAACGGTGCCGATTTGAGTGGT 901 AGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGG 612 72 421 192 432 492 481 552 661 g ò g ð g ò 유 g g 요 g ö ò ò ò ò g à ò 엽 d ò g ò 셤 à a ö g à 셤 ò 셤 ò g ð

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1081 CCCCCCGAGGTCAACAACAACACCTTGTCTTAATGATTGAACAAAATACCAAG 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A plasmid consisting of a pCMV4 expression vector including a coding sequence of human alpha-1 antitrypsin may be incorporated into liposomes capable of targeting specific tissue. The plasmid is then capable of expression of the gene extrachromosomally in the cells of the target tissue. Thus, the liposome including the plasmid can be used in a method for treating a deficiency of the plasmid can be used in a method for treating a deficiency of the gene product in cells of the target tissue. The specific use of the human alpha-1 antitrypsin is significant as this antiprotease is important in protecting the lungs against emphysema. The adult respiratory distress syndrome (ARRS) is thought
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 GAGGATCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCAC 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to involve a relative deficiency of antiprotease activity. Therefore, the delivery of a functioning alpha-1 antiprotease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human alpha-1 anti-trypsin contg. plasmid - for treatment of anti-protease deficiency in emphysema and other lung diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene to the lungs can be therapeutic in many human conditions
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                                                                                                                                                                                                                                                         Plasmid; pCMV4; liposome; antiprotease; lung; emphysema; adult respiratory distress syndrome; ARDS; ss.
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                                            1152 AGCCCATTGTTATGGGTAAGGTTGTCAACCCCAACTCAGAA 1192
                                                                       1141 TCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAA 1181
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60.2%;
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                                                                                                                                                                                                                                Human alpha-1 antitrypsin.
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Matches 711; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYVA-) UNIV VANDERBILT
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972 GITACIGAAGAAGCICCAITAAAATIGAGIAAAGCIGTICACAAAGCCGTCITAACTAIT 1031
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212 CIGGCACACCAACCAATATCTTCTCCCCAGTGAGCATCGCTACAGCC 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              672 ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA 731
                                                                       192 TICGCCATGITGAGITIAGGIACTAAAGCCGAIACCCAIGACGAGAITIIAGAAGGITIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     852 CGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTITAATITIGACCGAAATCCCAGAAGCCCCAAATITCACGAGGGTTTTCAAGAGTTGTTG
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyrold;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening for anti-neoplastic agent involves exposing cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endress G,
                                                        Thyroid cancer related gene sequence SEQ ID NO:5848.
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ABL67511 / Standard; DNA; 1352 BP
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2000US-233133P.
2000US-233617P.
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2000US-234034P.
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2000US-245084P.
                                        15-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Young PE, Augustus M
Soppet DR, Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AVAL-) AVALON PHARM.
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                                                                                stomach; lung;
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                                                                                                                   Homo sapiens
                                                                                                                                                                                    35-JUN-2000;
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                       ABL67511;
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anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (5) selected from 8447 sequences (given in AbL61664 to AbL70110), or is at least 95% identical to (5), where a change in expression is indicative of anti-neoplastic activity. (1) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, squamous cell carcinoma, neuroendocrine carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 CCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTTAGTCCTGTTTCTATTGCCACTGCT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 CTGGCACACCAGTCCAACAGCACCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCC 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 ITCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTA 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT 431
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chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 GIGGAGAAGGGIACICAAGGGAAAAIIGIGGAIIIGGICAAGGAGCIIGACAGAGACACA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 GTCTTCGCACTAGTTAACTATTTTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC
                                                                                                                 The present invention describes a method (M1) for screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.1%; Score 429; DB 24; Length 1352; 60.2%; Pred. No. 7.4e-98; Live 0; Mismatches 470; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1352 BP; 349 A; 386 C; 325 G; 292 T; 0 other;
                                                                   Claim 1; SEQ ID 5848; 44pp; English
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                                                          852 CGTCGTAGCGCTTCTCTGCCACTGCCAAGTTAAGTATCACCGGTACTTACGACTTAAAA 911
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